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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/495,448DATE: 02/23/2000  
TIME: 13:12:32

Input Set: I495448.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

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1 <110> APPLICANT: LAU, Lester F.  
2 <120> TITLE OF INVENTION: EXTRACELLULAR MATRIX SIGNALLING MOLECULES  
3 <130> FILE REFERENCE: 28758/36072  
4 <140> CURRENT APPLICATION NUMBER: US/09/495,448  
5 <141> CURRENT FILING DATE: 2000-01-31  
6 <150> EARLIER APPLICATION NUMBER: 09/142,569  
7 <151> EARLIER FILING DATE: 1999-04-02  
8 <150> EARLIER APPLICATION NUMBER: 60/013,958  
9 <151> EARLIER FILING DATE: 1996-03-15  
10 <160> NUMBER OF SEQ ID NOS: 32  
11 <170> SOFTWARE: PatentIn Ver. 2.0  
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15 <213> ORGANISM: Mus musculus  
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18 <222> LOCATION: (180)..(1316)  
19 <220> FEATURE:  
20 <223> OTHER INFORMATION: Mouse cyr61 cDNA coding sequence  
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24 ctcgcggct ttttgttct gtgtcgccgc gtcgcggcc gttccctctg cgcgccaca 179  
25 atg agc tcc agc acc ttc agg acg ctc gct gtc gcc acc ctt ctc 227  
26 Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu  
27 1 5 10 15  
28 cac ttg acc aga ctg gcg ctc tcc acc tgc ccc gcc gac tgc cac tgc 275  
29 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys  
30 20 25 30  
31 cct ctg gag gca ccc aag tgc gcc ccg gga gtc ggg ttg gtc cgg gac 323  
32 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp  
33 35 40 45  
34 ggc tgc ggc tgc tgt aag gtc tgc gct aaa caa ctc aac gag gac tgc 371  
35 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
36 50 55 60  
37 agc aaa act cag ccc tgc gac cac acc aag ggg ttg gaa tgc aat ttc 419  
38 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
39 65 70 75 80  
40 ggc gcc agc tcc acc gct ctg aaa ggg atc tgc aga gct cag tca gaa 467  
41 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu  
42 85 90 95  
43 ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa agc 515  
44 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser

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48	115	120	125	
49	ggc tgc att cct ctg tgt ccc caa gaa ctg tct ctc ccc aat ctg ggc			611
50	Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly			
51	130	135	140	
52	tgt ccc aac ccc cggtgtaaa gtc agc ggg cag tgc tgt gaa gag			659
53	Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu			
54	145	150	155	160
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58	gac ctc ctc gga ctc gat gcc tcg gag gtg gag tta acg aga aac aat			755
59	Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn			
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61	gag tta atc gca att gga aaa ggc agc tca ctg aag agg ctt cct gtc			803
62	Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val			
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64	ttt ggc acc gaa ccg cga gtt ctt ttc aac cct ctg cac gcc cat ggc			851
65	Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly			
66	210	215	220	
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74	Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln			
75	260	265	270	
76	cca gtg tac agc agc cta aaa aag ggc aag aaa tgc agc aag acc aag			1043
77	Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys			
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79	aaa tcc cca gaa cca gtc aga ttt act tat gca gga tgc tcc agt gtc			1091
80	Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val			
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82	aag aaa tac cgg ccc aaa tac tgc ggc tcc tgc gta gat ggc cgg tgc			1139
83	Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys			
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85	tgc aca cct ctg cag acc aga act gtg aag atg cgg ttc cga tgc gaa			1187
86	Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu			
87	325	330	335	
88	gat gga gag atg ttt tcc aag aat gtc atg atg atc cag tcc tgc aaa			1235
89	Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys			
90	340	345	350	
91	tgt aac tac aac tgc ccg cat ccc aac gag gca tcg ttc cga ctg tac			1283
92	Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr			
93	355	360	365	
94	agc cta ttc aat gac atc cac aag ttc agg gac taagtgcctc cagggttcct			1336

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95 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp  
96 370 375  
97 agtgtggct ggacagagga gaagcgcaag catcatggag acgtgggtgg gcggaggatg 1396  
98 aatgggcct tgctcattct tgagtagcat tagggtattt caaaactgcc aaggggctga 1456  
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Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp  
107 35 40 45  
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
108 50 55 60  
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
109 65 70 75 80  
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu  
110 85 90 95  
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser  
111 100 105 110  
Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val  
112 115 120 125  
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly  
113 130 135 140  
Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu  
114 145 150 155 160  
Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp  
115 165 170 175  
Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn  
116 180 185 190  
Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val  
117 195 200 205  
Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly  
118 210 215 220  
Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser  
119 225 230 235 240  
Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys  
120 245 250 255  
Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln  
121 260 265 270  
Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys  
122 275 280 285  
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123 290 295 300  
Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys  
124 305 310 315 320

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145 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu  
146 325 330 335  
147 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys  
148 340 345 350  
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159 <222> LOCATION: (124)..(1266)  
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165 aca atg agc tcc cgc atc gcc agg gcg ctc gcc tta gtc gtc acc ctt 168  
166 Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu  
167 1 5 10 15  
168 ctc cac ttg acc agg ctg gcg ctc tcc acc tgc ccc gct gcc tgc cac 216  
169 Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His  
170 20 25 30  
171 tgc ccc ctg gag gcg ccc aag tgc gcg ccg gga gtc ggg ctg gtc cgg 264  
172 Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg  
173 35 40 45  
174 gac ggc tgc ggc tgc tgt aag gtc tgc gcc aag cag ctc aac gag gac 312  
175 Asp Gly Cys Gly Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp  
176 50 55 60  
177 tgc agc aaa acg cag ccc tgc gac cac acc aag ggg ctg gaa tgc aac 360  
178 Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn  
179 65 70 75  
180 ttc ggc gcc agc tcc acc gct ctg aag ggg atc tgc aga gct cag tca 408  
181 Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser  
182 80 85 90 95  
183 gag ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa 456  
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185 100 105 110  
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188 115 120 125  
189 gtg ggc tgc att cct ctg tgt ccc caa gaa cta tct ctc ccc aac ttg 552  
190 Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu  
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192 ggc tgt ccc aac cct cgg ctg gtc aaa gtt acc ggg cag tgc tgc gag 600  
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198	gac ggc ctc ctt ggc aag gag ctg gga ttc gat gcc tcc gag gtg gag	696
199	Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu	
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201	ttg acg aga aac aat gaa ttg att gca gtt gga aaa ggc aga tca ctg	744
202	Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu	
203	195 200 205	
204	aag cgg ctc cct gtt ttt gga atg gag cct cgc atc cta tac aac cct	792
205	Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro	
206	210 215 220	
207	tta caa ggc cag aaa tgt att gtt caa aca act tca tgg tcc cag tgc	840
208	Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys	
209	225 230 235	
210	tca aag acc tgt gga act ggt atc tcc aca cga gtt acc aat gac aac	888
211	Ser Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn	
212	240 245 250 255	
213	cct gag tgc cgc ctt gtg aaa gaa acc cgg att tgt gag gtg cgg cct	936
214	Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro	
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216	tgt gga cag cca gtg tac agc agc ctg aaa aag ggc aag aaa tgc agc	984
217	Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser	
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224	305 310 315	
225	ggc cga tgc tgc acg ccc cag ctg acc agg act gtc aag atg cgg ttc	1128
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228	cgc tgc gaa gat ggg gag aca ttt tcc aag aac gtc atg atg atc cag	1176
229	Arg Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln	
230	340 345 350	
231	tcc tgc aaa tgc aac tac aac tgc ccg cat gcc aat gaa gca gcg ttt	1224
232	Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe	
233	355 360 365	
234	ccc ttc tac agg ctg ttc aat gac att cac aaa ttt agg gac	1266
235	Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp	
236	370 375 380	
237	taaatgtac ctgggttcc agggcacacc tagacaaaaca agggagaaga gtgtcagaat	1326
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VERIFICATION SUMMARY  
PATENT APPLICATION US/09/495,448

DATE: 02/23/2000  
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Input Set: I495448.RAW

Line ? Error/Warning

Original Text

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